

**FIGURE 1****HMMGENE FOR NT\_006302.5**

Peptide VMLMIQETNK (SEQ ID NO:18, frame = 1)

Predictions :

1223361-1223403 +  
1224023-1224114 + VMLMIQETNK

Score = 0.158

>NT\_006302.5

MALSLSSSKRLQLDNRVMLMIQETNKQKVKGSGPYRNMTVTQMS\*

**FIGURE 2****HMMGENE FOR NT\_006431.5**

Peptide LLNNFPYR (SEQ ID NO:20, frame = 1)

Predictions :

2323834-2323931 +  
2350894-2350927 +  
2351807-2351866 +  
2363588-2363659 + LLNNFPYR

Score = 0.019

>NT\_006431.5

MISRQIGCRVYEDLRLISKFFVISNCKDETAINGFYFGKNSIYGKVIEKTDEEIRSLFYEFPQTLLNNFPYREVLWSLPVPRSSDRK\*

**FIGURE 3****HMMGENE FOR NT\_007712.5**

Peptide SGCTNLRSHQQCIR (SEQ ID NO:27, frame = 3)

Predictions :

116490-116500 +

121555-121669 + SGCTNLRSHQQCIR

Score = 0.081

>NT\_007712.5

MLASN SIFHFLRTLQTVLRSGCTNLRSHQQCIRVPFSPHPQ\*

**FIGURE 4****HMMGENE FOR NT\_007914.5**

Peptide ESIYFIIAAMLVATK (SEQ ID NO:31, frame = 1)

Predictions :

1365933-1366033 +

1374991-1375117 + ESIYFIIAAMLVATK

Score = 0.137

>NT\_007914.5

MHRKDNGEMSGEAGKAGTPKGEGHGKKPTHVISYSSSKRKSLFFWKEESIYFIIAAMLV  
ATKAANQIYEGQPTQS\*

**FIGURE 5****HMMGENE FOR NT\_009891.1**

Peptide QADGTVFSK (SEQ ID NO:47, frame = 3)

Predictions :

995796-995822 +  
1001710-1001787 + QADGTVFSK

Score = 0.080

>NT\_009891.1

MIKTESKSKYLSFTSFKQADGTVFSKMKRKHLK\*

**FIGURE 6****HMMGENE FOR NT\_010909.5**

Peptide CVIFPLNSYGMLLK (SEQ ID NO:53, frame = 3)

Predictions :

146623-146704 +  
164675-164798 +  
176327-176399 +  
177711-177772 +  
183840-183972 +  
184830-184912 + CVIFPLNSYGMLLK  
185665-185759 +  
195917-196005 +  
197742-198041 +

Score = 0.000

>NT\_010909.5

MAFPDHKDAGKCSHLFSPVGEEREVKIGVPAVFCSCPCYVAELCCPILSRAPKPPDPVA  
AEHLNHGQSRSDELSAYVSTYLVPGNVLGTGDPMTEDPTMERPYTFKDFLLPRRDVSS  
ESDNNIRQINQEAAHRRFRSRRHISEDLEPEPSEGVDVPEIYYHENINLGEOKCVIFPL  
NSYGMLLKTISDQPSGAVRGTKQKASDHSLQWGTVQLFDCWEERDAKGRTYYVNHN  
RTTTWTRPIMQGAKDSPVRAVKDTLSNPQSPQSPYNSPKPQHKVTQSFLPPGWEMRI  
APNGRPFFIDHNTKTTWVRLLLLFGSIFIMKSGINSLISLVFVVLAELD\*

**FIGURE 7****HMMGENE FOR NT\_011896.6**

Peptide EAEFESTMQK ( SEQ ID NO:62, frame = 1)

Predictions :

1531370-1531413 +  
1550835-1550907 +  
1558914-1559284 +  
1580914-1580962 + EAEFESTMQK  
1590737-1590816 +  
1609576-1609750 +  
Score = 0.000

>NT\_011896.6

MRKGSEVV CYQQEQQNESEGPMLSFD FSRNEL SNGMAQARI KYLGIQLVRVGKD LFKEN  
YEPLFEKIREDENKWKNIPYSWIGTINIVKMAILPKVIYRFNATLIELPW AFFTELEKT  
TLKFIWNQKRAHI AKKILSKKNAGGIMLPDFKLYYKGTVTKA WAVTFAKEA EFESTM  
QKDSSCSPAMEQS WTENDFDELTEVGFRNIITITIIFTITIIITITI ITVIITMII  
TIIMTIITNTIITITIII IMIITIIT\*

**FIGURE 8****HMMGENE FOR NT\_019265.5**

Peptide QVQSYHVLGK (SEQ ID NO:66, frame = 1)

Predictions :

745567-745650 +  
749487-749540 + QVQSYHVLGK  
Score = 0.014  
>NT\_019265.5

MAKPHIYPKYKNYLGV EALACGPTWKAEQVQSYHVLGK QRTNHIG\*

**FIGURE 9****HMMGENE FOR NT\_022148.5**

Peptide CLCTHNGASKYMK (SEQ ID NO:73, frame = 1)

Predictions :

513123-513179 +

517522-517632 +

524582-524606 +

530347-530459 + CLCTHNGASKYMK

Score = 0.033

>NT\_022148.5

MDLTLLETHLESYRISSQMPSFLLPLGQGGSTVIRDNVDPQKRAADLQESGQTIFQRKT  
KTSEEGVNSPRRHNNPKCLCTHNGASKYMKQKHTEPDTSQLY\*

**FIGURE 10****HMMGENE FOR NT\_022851.5**

Peptide EQNKILSNLEIER (SEQ ID NO:76, frame = 3)

Predictions :

187415-187484 + EQNKILSNLEIER

191445-191529 +

202588-202654 +

203509-203661 +

204036-204245 +

Score = 0.023

>NT\_022851.5

MEQDTKELKEEQNKILSNLEIERDKEEAETQRNYEIFPRTCKCYELEPECKSRYQHLSEE  
AEDMGLVVICPYLSEAAQSPQVFECIWSFLQISLVFISQNNLELVEISGKTLQDDYVTI  
ARVICDQGGRVVNFGISWKLEVRLRDGKSCPQDPEKDSKEQPNLTEGEKAKGAVCKN  
QISWSLASAKLLCVGRV\*

**FIGURE 11****HMMGENE FOR NT\_007897.5**

Peptide TEGLTLLQLV (SEQ ID NO:30, frame = 2)

Predictions :

1266436-1266537 + TEGLTLLQLV

Score = 0.108

>NT\_007897.5

MDKRREAGNRESRISPGRVAGGRTEGLTLLQLV\*

**FIGURE 12****HMMGENE FOR NT\_009561.5**

Peptide MKPLVDYK (SEQ ID NO:43, frame = 1)

Predictions :

800421-800456 +

802726-802910 +

803769-803924 +

813981-814042 +

820146-820240 +

833001-833030 + MKPLVDYK

Score = 0.025

>NT\_009561.5

MDMHRDKVYNEQGLIHLFVAENEVSLFSSLVLCFPMRKKEKTPDGEHQIVGRFETP  
LEFVLVMQSLVQTDNKTAFSNDNSYKSRLSDKLPSVPLPAWMHSWNLAHKGIRIAFRQ  
CFNHPKSRMYQSSLANTVLCASFDYLFRDEEPGLSNICTFSSRLVQKVQLTATEGLLS  
IRMKPLVDYK\*

FIGURE 13**HMMGENE FOR NT\_011387.5**

Peptide DSYLNVKR (SEQ ID NO:55, frame = 2)

Predictions :

16190762-16190828 +  
16193267-16193291 +  
16197014-16197074 +  
16205986-16206098 +  
16210646-16210725 +  
16212833-16212956 +  
16214152-16214188 + DSYLNVKR

Score = 0.004

>NT\_011387.5

MHNSPTVTTQYSLTDEWIIKWVMIYQRNQGNNSRGSGFTFWLGDYKHSVDPSIASPS  
PEAAALCVPDDNLGIGTNQYQEWCWERALRLTRMDSINQAPLPCILSCIGAMEATALL  
RPVSCLTFRKCVDYFWLRVEREIAWERKSSYECQLNFGCFYKDSYLNKR\*

FIGURE 14**HMMGENE FOR NT\_027064.2**

Peptide PEMVVQACSLSY (SEQ ID NO:96, frame = 3)

Predictions :

553561-553602 +  
578259-578297 + PEMVVQACSLSY  
Score = 0.027  
>NT\_027064.2  
MGKGWEVYNRQDLQPEMVVQACSLSY\*

**FIGURE 15****HMMGENE FOR NT\_028428.2**

Peptide NAKISQAPW (SEQ ID NO:102, frame = 1)

Predictions :

290705-290780 +

296029-296147 + NAKISQAPW

Score = 0.091

&gt;NT\_028428.2

MDASVGHYPKKINTGMENQVPHVLASLWEAEVGESPEVRSSKPDWPRWQNPISTKNAKI  
SQAPW\***FIGURE 16****HMMGENE FOR NT\_019546.5**

Peptide NPMKIFEK (SEQ ID NO:67, frame = 1)

Predictions :

611472-611544 + NPMKIFEK

612968-613179 +

Score = 0.475

&gt;NT\_019546.5

MMLRNNPMKIFEKRKYIPQQKMLQK\*